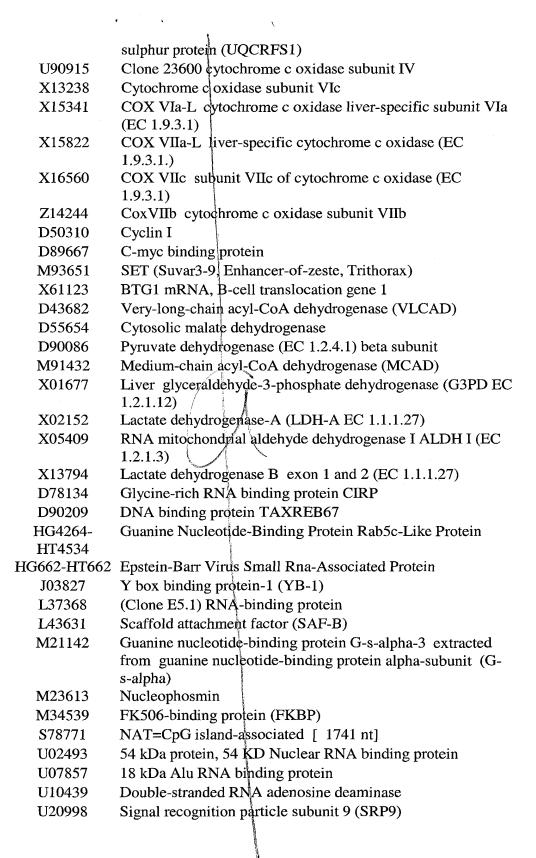
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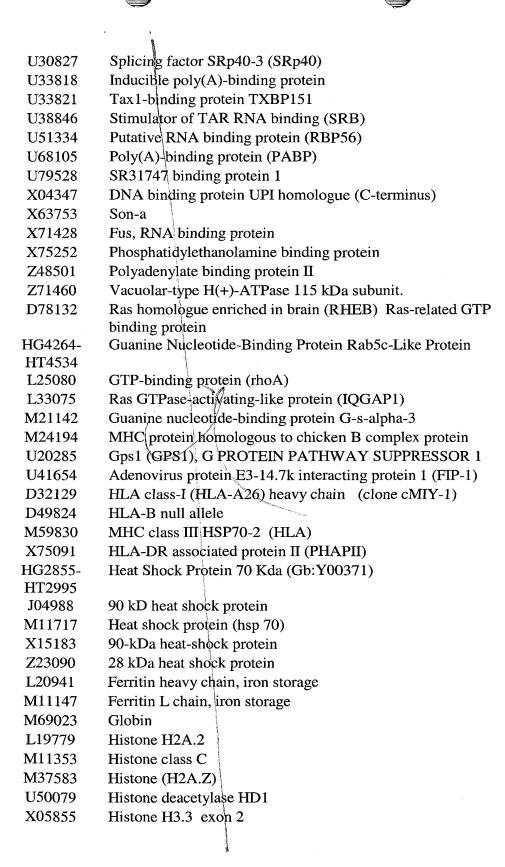
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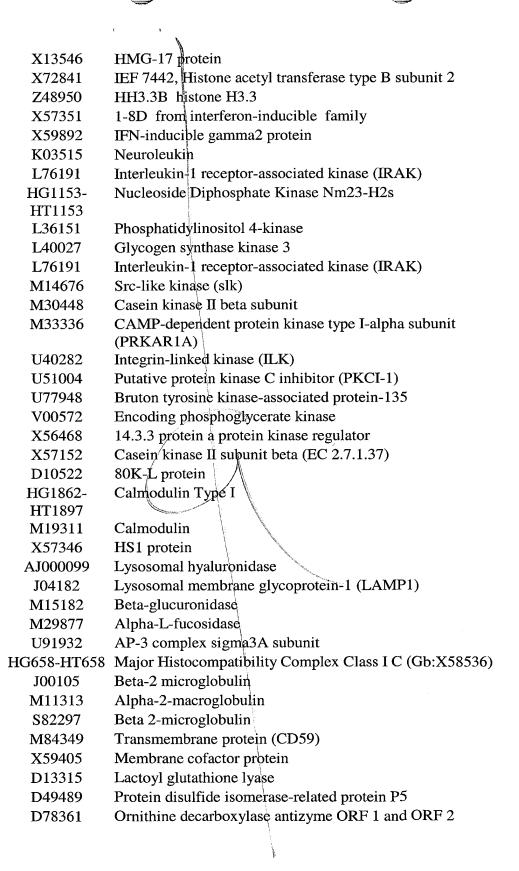
- A method for identifying a maintenance gene comprising:
 determining the expression of at least one hundred genes in at least two different
 types of tissues in two different developmental stages; and
 indicating a gene that is expressed at the same level in said tissues in said stages
 as said maintenance gene.
 - 2. The method of Claim 1 wherein said at least one hundred genes comprise at least one thousand genes.
 - 3. The method of Claim 1 wherein said at least two types of tissues comprise at least five different types of tissues.
 - 4. The method of Claim 1 wherein said determining uses nucleic acid probe arrays.
 - 5. The method of Claim 1 wherein a gene is considered as expressed at the same level if the variation of its expression is within 10 fold.
 - 6. The method of Claim 5 wherein a gene is considered as expressed at the same level if the variation of its expression is within 5 fold.
 - 7. The method of Claim 6 wherein a gene is considered as expressed at the same level if the variation of its expression is within 2 fold.
- 8. The method of Claim 1 wherein a gene is considered as expressed at the same level if the variation of its expression is not statistically significant.
 - 9. A method for comparing the expression of a gene in a plurality of biological samples comprising:

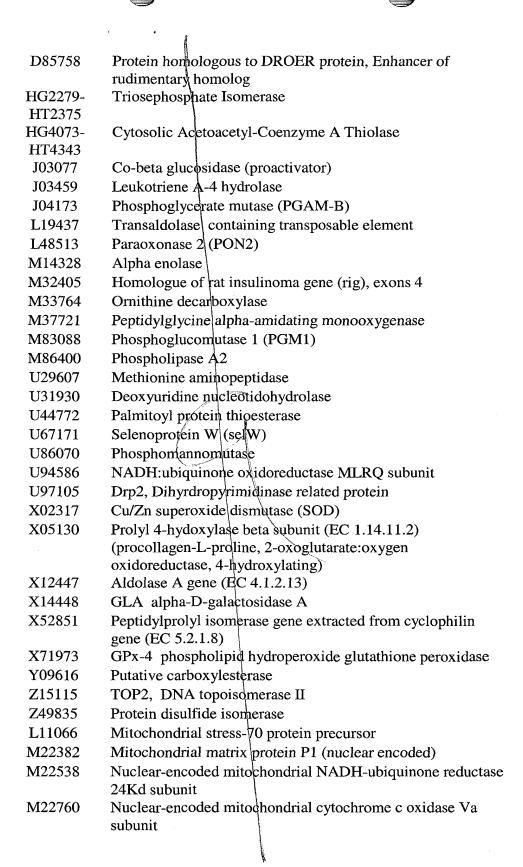
measuring the expression of at least three maintenance genes selected from the group consisted of:

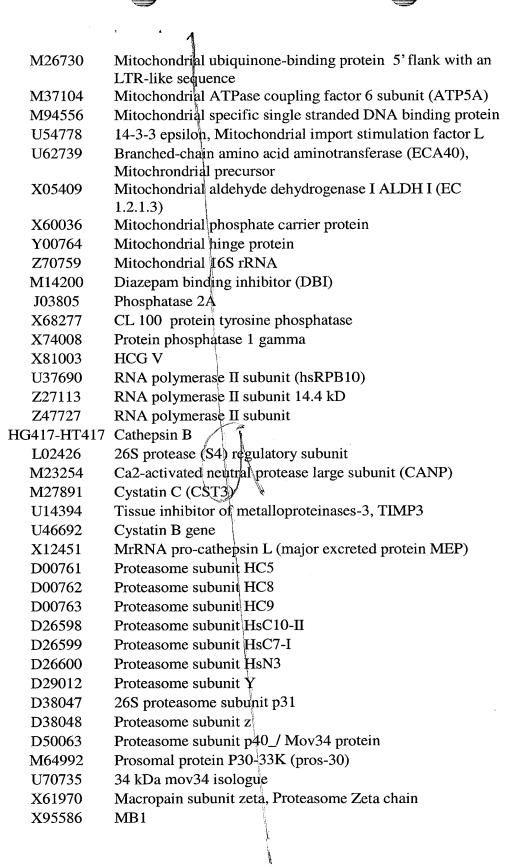
HG2815-	Myosin, Light Chain, Alkali, (Gb: U02629), Alt. Splice 2
HT2931 J03191	Profilin
M10277	Cytoplasmic beta-actin
M10277 M14483	· · ·
	PTMA gene extracted from prothymosin alpha
M17733	Thymosin beta-4 mRNA
M19283	Cytoskeletal gamma-actin
M26708	Prothymosin alpha mRNA (ProT-alpha)
S65738	Actin depolymerizing factor
U37122	Adducin gamma subunit
X00351	Beta-actin
X54304	Myosin regulatory light chain
X95404	Non-muscle type cofilin
D15057	DAD-1
L08246	Myeloid cell differentiation protein (MCL1)
M63379	TRPM-2 protein, Clusterin
D13118	ATP synthase subunit c encoded by P1
D14710	ATP synthase alpha subunit
D16469	Vacuolar ATP synthase subunit AC45 precursor
D16562	ATP synthase gamma-subunit (L-type)
D49400	Fetus brain vacuolar ATPase
M19483	ATP synthase beta subunit
M37104	Mitochondrial ATPase coupling factor 6 subunit (ATP5A)
U09813	Mitochondrial ATP synthase subunit 9, P3 gene copy
U16799	NaK-ATPase beta-1 subunit
U51478	Sodium/potassium-transporting ATPase beta-3 subunit
X60221	H+-ATP synthase subunit b
X64330	ATP-citrate lyase
X83218	ATP synthase
Z71460	Vacuolar-type H(+)-ATPase 115 kDa subunit
AB001325	AQP3 aquaporine 3 (water channel)
L06132	Voltage-dependent anion channel isoform 1 (VDAC)
L08666	Porin (por)
AC002115	COX6B (COXG)
J04823	Cytochrome c oxidase subunit VIII (COX8)
J04973	Cytochrome bc-1 complex core protein II
L32977	Clone f17252 ubiquinol cytochrome c reductase Rieske iron-
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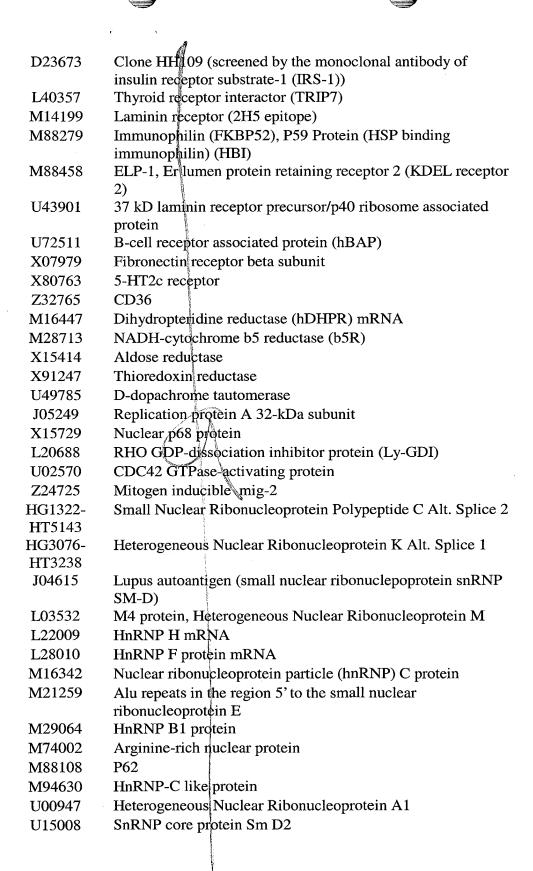


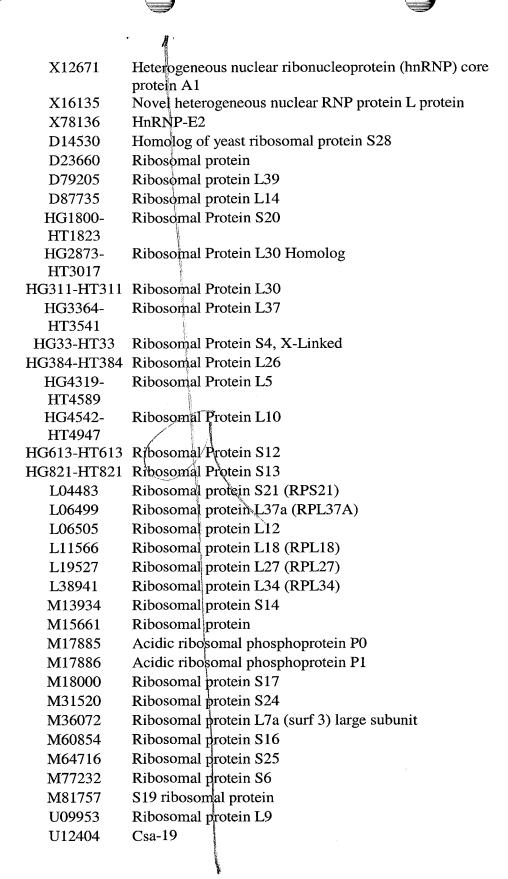


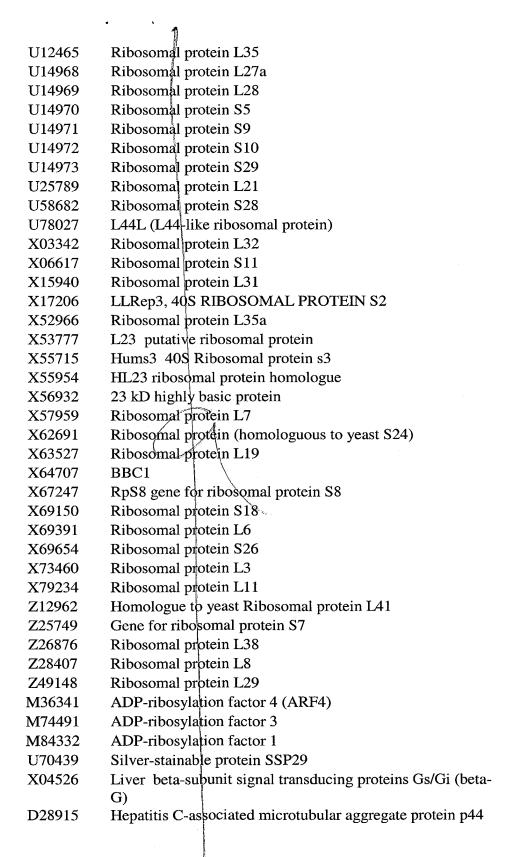


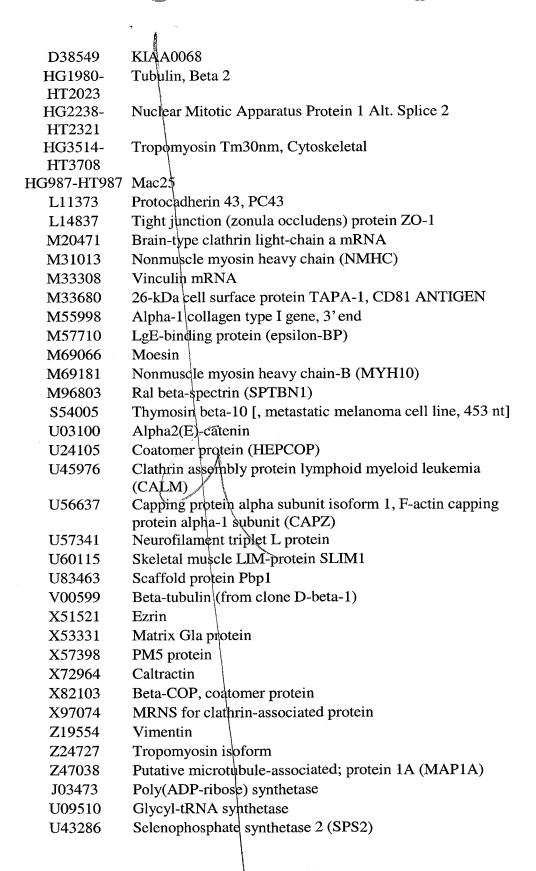


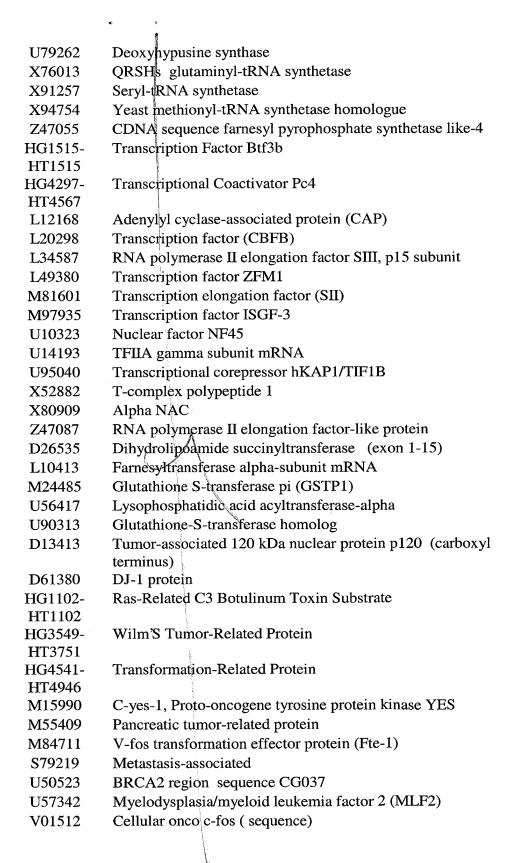


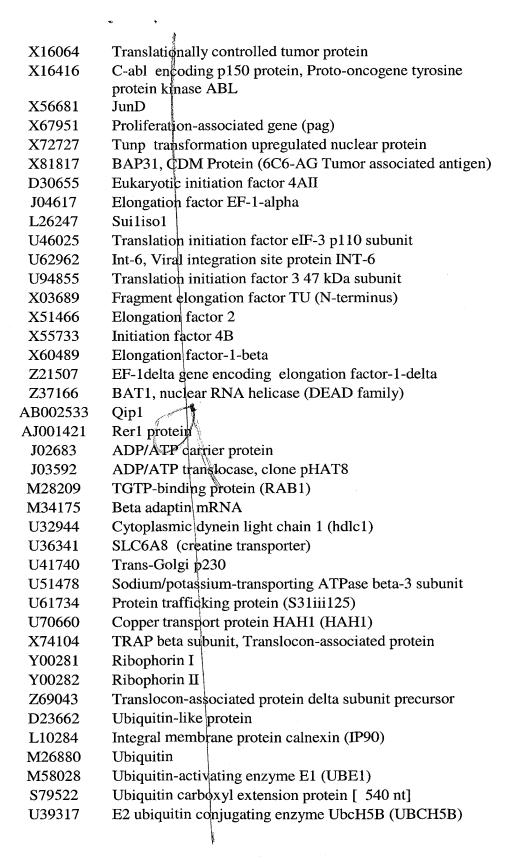


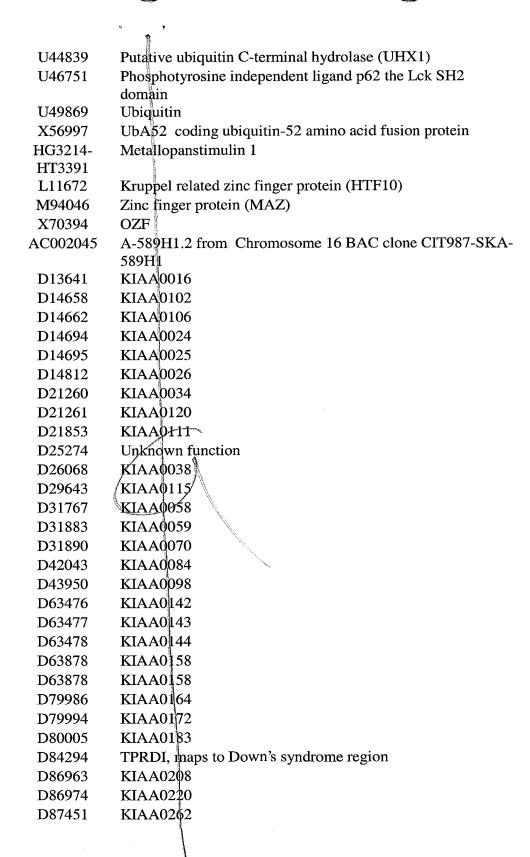


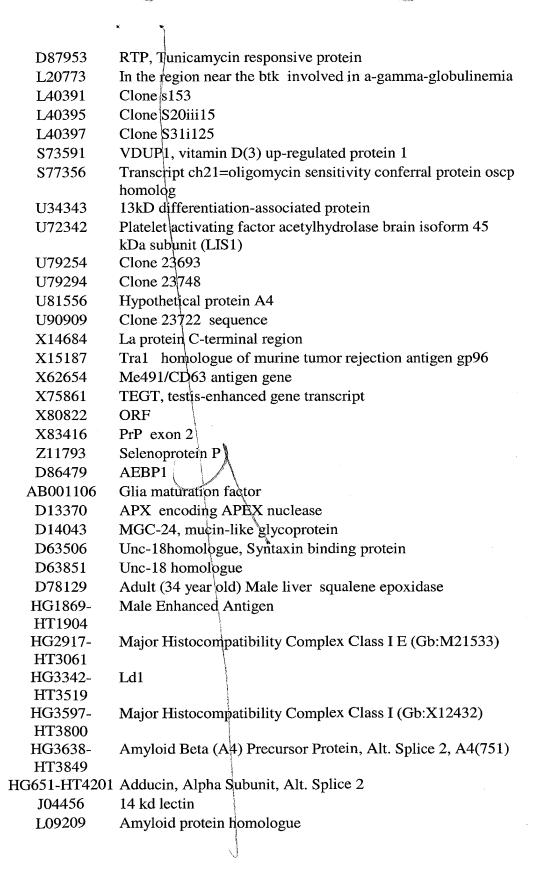


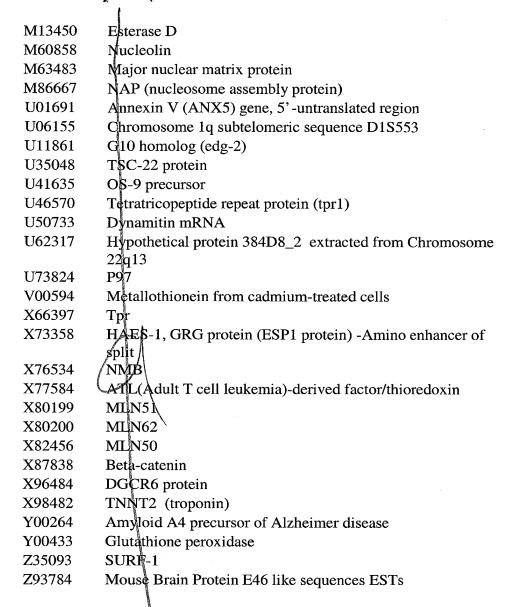










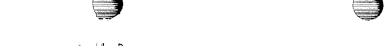


and

evaluating said expression of said gene in said plurality of samples using the expression of said at least three maintenance genes.



10. The method of Claim 9 wherein said at least three maintenance genes comprise at least five maintenance genes selected from said group.



- 11. The method of Claim 10 wherein said at least five maintenance genes comprise at least ten maintenance genes selected from said group.
- The method of Claim 9 wherein said evaluating comprises calculating expression ratio of said gene over said maintenance genes.

